RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/557,823*

INPUT SET: S35718.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANTS: Bucala, Richard J. et al.

(ii) TITLE OF INVENTION: Inhibition of Migration Inhibitory Factor in the Treat Cytokine-Mediated Toxicity

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
(B) STREET: 2600 Century Square, 1501 Fourth Avenue
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: U.S.A.
(F) ZIP: 98101-1688

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows95
(D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: to be assigned**
(B) FILING DATE: 24 April 2000
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Oster, Jeffrey B.
(B) REGISTRATION NUMBER: 32,585
(C) REFERENCE/DOCKET NUMBER: 0203H

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 206 628-7711
(B) TELEFAX: 206 628-7699

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCCTATGT TCATCGTGAA CACCAATGTT CCCCGCGCCT CCGTGCCAGA GGGGTTTCTG 60

TCGGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCGCACAGTA CATCGCAGTG 120

CACGTGGTCC CGGACCAGCT CATGACTTTT AGCGGCACGA ACGATCCCTG CGCCCTCTGC 180

AGCCTGCACA GCATCGGCAA GATCGGTGGT GCCCAGAACC GCAACTACAG TAAGCTGCTG 240

TGTGGCCTGC TGTCCGATCG CCTGCACATC AGCCCGGACC GGGTCTACAT CAACTATTAC 300

GACATGAACG CTGCCAACGT GGGCTGGAAC GGTTCCACCT TCGCTTGA 348

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCCGATGT TCATCGTAAA CACCAACGTG CCCCGCGCCT CCGTGCCGGA CGGGTTCCTC 60

TCCGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCCCCCAGTA CATCGCGGTG 120

CACGTGGTCC CGGACCAGCT CATGGCCTTC GGCGGCTCCA GCGAGCCGTG CGCGCTCTGC 180

AGCCTGCACA GCATCGGCAA GATCGGCGGC GCGCAGAACC GCTCCTACAG CAAGCTGCTG 240

TGCGGCCTGC TGGCCGAGCG CCTGCGCATC AGCCCGGACA GGGTCTACAT CAACTATTAC 300

GACATGAACG CGGCCAGTGT GGGCTGGAAC AACTCCACCT TCGCCTAA 348

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATGCCTAT GTTCATCGTG AACACCAATG TTCCCCGCGC CTCCGTGCCA GAGGGGTTTC 60

TGTCGGAGCT CACCCAGCAG CTGGCGCAGG CCACCGGCAA GCCCGCACAG TACATCGCAG 120

TGCACGTGGT CCCGGACCAG CTCATGACTT TTAGCGGCAC GAACGATCCC TGCGCCCTCT 180

GCAGCCTGCA CAGCATCGGC AAGATCGGTG GTGCCCAGAA CCGCAACTAC AGTAAGCTGC 240

TGTGTGGCCT GCTGTCCGAT CGCCTGCACA TCAGCCCGGA CCGCTCCTAC AGCAAGCTGC 300

TGTGCGGCCT GCTGGCCGAG CGCCTGCGCA TCAGCCCGGA CCGGGTCTAC ATCAACTATT 360

ACGACATGAA CGCTGCCAAC GTGGGCTGGA ACGGTTCCAC CAGGGTCTAC ATCAACTATT 420

ACGACATGAA CGCGGCCAGT GTGGGCTGGA ACAACTCCAC CTTCGCTTGA GTCCTGGCCC 480

CACTTACCTG CACCGCTGTT C 501

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro
1 5 10 15

Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly
20 25 30

Lys Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met
35 40 45

Thr Phe Ser Gly Thr Asn Asp Pro Cys Ala Leu Cys Ser Leu His Ser
50 55 60

Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu
65 70 75 80

Cys Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr
85 90 95

Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser

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153                 100                 105                 110
154
155       Thr Phe Ala
156               115
157
158
159   (2) INFORMATION FOR SEQ ID NO:5:
160
161        (i) SEQUENCE CHARACTERISTICS:
162             (A) LENGTH: 115 amino acids
163             (B) TYPE: amino acid
164             (C) STRANDEDNESS: single
165             (D) TOPOLOGY: unknown
166
167       (ii) MOLECULE TYPE: peptide
168
169      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
170
171       Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro
172       1               5                   10                  15
173
174       Asp Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly
175                   20                  25                  30
176
177       Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met
178               35                  40                  45
179
180       Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser
181           50                  55                  60
182
183       Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu
184       65                  70                  75                  80
185
186       Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr
187                       85                  90                  95
188
189       Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser
190                   100                 105                 110
191
192       Thr Phe Ala
193               115
194
195
196   (2) INFORMATION FOR SEQ ID NO:6:
197
198        (i) SEQUENCE CHARACTERISTICS:
199             (A) LENGTH: 9 amino acids
200             (B) TYPE: amino acid
201             (C) STRANDEDNESS: single
202             (D) TOPOLOGY: unknown
203
204       (ii) MOLECULE TYPE: peptide
205
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Lys Lys Gly Ala Val Gly Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 15
(D) OTHER INFORMATION: /label= X
/note= "X = Asn or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ile Xaa His Asn Thr Val Ala Thr Glu Ile Ser Gly Tyr Asn Xaa Ala
1 5 10 15

Met

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATATGCCG ATGTTCATCG TAAACAC 27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/557,823*

DATE: 07/25/2000
TIME: 02:08:07

INPUT SET: S35718.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: to be assigned